

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Conkling, Mark A.  
Mendu, Nandini  
Song, Wen
- (ii) TITLE OF INVENTION: Regulation of Quinolate Phosphoribosyl  
Transferase Expression
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Kenneth Sibley, Bell Seltzer Park & Gibson
  - (B) STREET: Post Office Drawer 34009
  - (C) CITY: Charlotte
  - (D) STATE: North Carolina
  - (E) COUNTRY: USA
  - (F) ZIP: 28234
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Sibley, Kenneth D.
  - (B) REGISTRATION NUMBER: 31,665
  - (C) REFERENCE/DOCKET NUMBER: 5051-338P
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 919-420-2200
  - (B) TELEFAX: 919-881-3175

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1399 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 52..1104

(xi.) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAAAAACTAT TTTCCACAAA ATTCATTTC	CAACCCCCC	AAAAAAAAAC C	ATG TTT	57
			Met Phe	
			1	
AGA GCT ATT CCT TTC ACT GCT ACA GTG CAT CCT TAT GCA ATT ACA GCT				105
Arg Ala Ile Pro Phe Thr Ala Thr Val His Pro Tyr Ala Ile Thr Ala				
	5	10	15	
CCA AGG TTG GTG GTG AAA ATG TCA GCA ATA GCC ACC AAG AAT ACA AGA				153
Pro Arg Leu Val Val Lys Met Ser Ala Ile Ala Thr Lys Asn Thr Arg				
	20	25	30	
GTG GAG TCA TTA GAG GTG AAA CCA CCA GCA CAC CCA ACT TAT GAT TTA				201
Val Glu Ser Leu Glu Val Lys Pro Pro Ala His Pro Thr Tyr Asp Leu				
	35	40	45	50
AAG GAA GTT ATG AAA CTT GCA CTC TCT GAA GAT GCT GGG AAT TTA GGA				249
Lys Glu Val Met Lys Leu Ala Leu Ser Glu Asp Ala Gly Asn Leu Gly				
	55	60	65	
GAT GTG ACT TGT AAG GCG ACA ATT CCT CTT GAT ATG GAA TCC GAT GCT				297
Asp Val Thr Cys Lys Ala Thr Ile Pro Leu Asp Met Glu Ser Asp Ala				
	70	75	80	
CAT TTT CTA GCA AAG GAA GAC GGG ATC ATA GCA GGA ATT GCA CTT GCT				345
His Phe Leu Ala Lys Glu Asp Gly Ile Ile Ala Gly Ile Ala Leu Ala				
	85	90	95	
GAG ATG ATA TTC GCG GAA GTT GAT CCT TCA TTA AAG GTG GAG TGG TAT				393
Glu Met Ile Phe Ala Glu Val Asp Pro Ser Leu Lys Val Glu Trp Tyr				
	100	105	110	
GTA AAT GAT GGC GAT AAA GTT CAT AAA GGC TTG AAA TTT GGC AAA GTA				441
Val Asn Asp Gly Asp Lys Val His Lys Gly Leu Lys Phe Gly Lys Val				
	115	120	125	130
CAA GGA AAC GCT TAC AAC ATT GTT ATA GCT GAG AGG GTT GTT CTC AAT				489
Gln Gly Asn Ala Tyr Asn Ile Val Ile Ala Glu Arg Val Val Leu Asn				
	135	140	145	
TTT ATG CAA AGA ATG AGT GGA ATA GCT ACA CTA ACT AAG GAA ATG GCA				537
Phe Met Gln Arg Met Ser Gly Ile Ala Thr Leu Thr Lys Glu Met Ala				
	150	155	160	
GAT GCT GCA CAC CCT GCT TAC ATC TTG GAG ACT AGG AAA ACT GCT CCT				585
Asp Ala Ala His Pro Ala Tyr Ile Leu Glu Thr Arg Lys Thr Ala Pro				
	165	170	175	

GGA TTA CGT TTG GTG GAT AAA TGG GCG GTA TTG ATC GGT GGG GGG AAG Gly Leu Arg Leu Val Asp Lys Trp Ala Val Leu Ile Gly Gly Gly Lys 180 185 190	633
AAT CAC AGA ATG GGC TTA TTT GAT ATG GTA ATG ATA AAA GAC AAT CAC Asn His Arg Met Gly Leu Phe Asp Met Val Met Ile Lys Asp Asn His 195 200 205 210	681
ATA TCT GCT GCT GGA GGT GTC GGC AAA GCT CTA AAA TCT GTG GAT CAG Ile Ser Ala Ala Gly Gly Val Gly Lys Ala Leu Lys Ser Val Asp Gln 215 220 225	729
TAT TTG GAG CAA AAT AAA CTT CAA ATA GGG GTT GAG GTT GAA ACC AGG Tyr Leu Glu Gln Asn Lys Leu Gln Ile Gly Val Glu Val Glu Thr Arg 230 235 240	777
ACA ATT GAA GAA GTA CGT GAG GTT CTA GAC TAT GCA TCT CAA ACA AAG Thr Ile Glu Glu Val Arg Glu Val Leu Asp Tyr Ala Ser Gln Thr Lys 245 250 255	825
ACT TCG TTG ACT AGG ATA ATG CTG GAC AAT ATG GTT GTT CCA TTA TCT Thr Ser Leu Thr Arg Ile Met Leu Asp Asn Met Val Val Pro Leu Ser 260 265 270	873
AAC GGA GAT ATT GAT GTA TCC ATG CTT AAG GAG GCT GTA GAA TTG ATC Asn Gly Asp Ile Asp Val Ser Met Leu Lys Glu Ala Val Glu Leu Ile 275 280 285 290	921
AAT GGG AGG TTT GAT ACG GAG GCT TCA GGA AAT GTT ACC CTT GAA ACA Asn Gly Arg Phe Asp Thr Glu Ala Ser Gly Asn Val Thr Leu Glu Thr 295 300 305	969
GTA CAC AAG ATT GGA CAA ACT GGT GTT ACC TAC ATT TCT AGT GGT GCC Val His Lys Ile Gly Gln Thr Gly Val Thr Tyr Ile Ser Ser Gly Ala 310 315 320	1017
CTG ACG CAT TCC GTG AAA GCA CTT GAC ATT TCC CTG AAG ATC GAT ACA Leu Thr His Ser Val Lys Ala Leu Asp Ile Ser Leu Lys Ile Asp Thr 325 330 335	1065
GAG CTC GCC CTT GAA GTT GGA AGG CGT ACA AAA CGA GCA TGAGCGCCAT Glu Leu Ala Leu Glu Val Gly Arg Arg Thr Lys Arg Ala 340 345 350	1114
TACTTCTGCT ATAGGGTTGG AGTAAAAGCA GCTGAATAGC TGAAAGGTGC AAATAAGAAT	1174
CATTTTACTA GTTGTCAAAC AAAAGATCCT TCACTGTGTA ATCAAACAAA AAGATGTAAA	1234
TTGCTGGAAT ATCTCAGATG GCTCTTTTCC AACCTTATTG CTTGAGTTGG TAATTTTATT	1294
ATAGCTTTGT TTTTCATGTTT CATGGAATTT GTTACAATGA AAATACTTGA TTTATAAGTT	1354
TGGTGTATGT AAAATTCTGT GTTACTTCAA ATATTTTGAG ATGTT	1399

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Phe Arg Ala Ile Pro Phe Thr Ala Thr Val His Pro Tyr Ala Ile  
 1 5 10 15  
 Thr Ala Pro Arg Leu Val Val Lys Met Ser Ala Ile Ala Thr Lys Asn  
 20 25 30  
 Thr Arg Val Glu Ser Leu Glu Val Lys Pro Pro Ala His Pro Thr Tyr  
 35 40 45  
 Asp Leu Lys Glu Val Met Lys Leu Ala Leu Ser Glu Asp Ala Gly Asn  
 50 55 60  
 Leu Gly Asp Val Thr Cys Lys Ala Thr Ile Pro Leu Asp Met Glu Ser  
 65 70 75 80  
 Asp Ala His Phe Leu Ala Lys Glu Asp Gly Ile Ile Ala Gly Ile Ala  
 85 90 95  
 Leu Ala Glu Met Ile Phe Ala Glu Val Asp Pro Ser Leu Lys Val Glu  
 100 105 110  
 Trp Tyr Val Asn Asp Gly Asp Lys Val His Lys Gly Leu Lys Phe Gly  
 115 120 125  
 Lys Val Gln Gly Asn Ala Tyr Asn Ile Val Ile Ala Glu Arg Val Val  
 130 135 140  
 Leu Asn Phe Met Gln Arg Met Ser Gly Ile Ala Thr Leu Thr Lys Glu  
 145 150 155 160  
 Met Ala Asp Ala Ala His Pro Ala Tyr Ile Leu Glu Thr Arg Lys Thr  
 165 170 175  
 Ala Pro Gly Leu Arg Leu Val Asp Lys Trp Ala Val Leu Ile Gly Gly  
 180 185 190  
 Gly Lys Asn His Arg Met Gly Leu Phe Asp Met Val Met Ile Lys Asp  
 195 200 205  
 Asn His Ile Ser Ala Ala Gly Gly Val Gly Lys Ala Leu Lys Ser Val  
 210 215 220  
 Asp Gln Tyr Leu Glu Gln Asn Lys Leu Gln Ile Gly Val Glu Val Glu  
 225 230 235 240

Thr Arg Thr Ile Glu Glu Val Arg Glu Val Leu Asp Tyr Ala Ser Gln  
 245 250 255  
 Thr Lys Thr Ser Leu Thr Arg Ile Met Leu Asp Asn Met Val Val Pro  
 260 265 270  
 Leu Ser Asn Gly Asp Ile Asp Val Ser Met Leu Lys Glu Ala Val Glu  
 275 280 285  
 Leu Ile Asn Gly Arg Phe Asp Thr Glu Ala Ser Gly Asn Val Thr Leu  
 290 295 300  
 Glu Thr Val His Lys Ile Gly Gln Thr Gly Val Thr Tyr Ile Ser Ser  
 305 310 315 320  
 Gly Ala Leu Thr His Ser Val Lys Ala Leu Asp Ile Ser Leu Lys Ile  
 325 330 335  
 Asp Thr Glu Leu Ala Leu Glu Val Gly Arg Arg Thr Lys Arg Ala  
 340 345 350

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGTTTAGAG CTATTCCTTT CACTGCTACA GTGCATCCTT ATGCAATTAC AGCTCCAAGG	60
TTGGTGGTGA AAATGTCAGC AATAGCCACC AAGAATACAA GAGTGGAGTC ATTAGAGGTG	120
AAACCACCAG CACACCCAAC TTATGATTTA AAGGAAGTTA TGAAACTTGC ACTCTCTGAA	180
GATGCTGGGA ATTTAGGAGA TGTGACTTGT AAGGCGACAA TTCCTCTTGA TATGGAATCC	240
GATGCTCATT TTCTAGCAAA GGAAGACGGG ATCATAGCAG GAATTGCACT TGCTGAGATG	300
ATATTCGCGG AAGTTGATCC TTCATTAAAG GTGGAGTGGT ATGTAAATGA TGGCGATAAA	360
GTTCATAAAG GCTTGAAATT TGGCAAAGTA CAAGGAAACG CTTACAACAT TGTTATAGCT	420
GAGAGGGTTG TTCTCAATTT TATGCAAAGA ATGAGTGGAA TAGCTACACT AACTAAGGAA	480
ATGGCAGATG CTGCACACCC TGCTTACATC TTGGAGACTA GGAAAACTGC TCCTGGATTA	540
CGTTTGGTGG ATAAATGGGC GGTATTGATC GGTGGGGGGA AGAATCACAG AATGGGCTTA	600

TTTGATATGG TAATGATAAA AGACAATCAC ATATCTGCTG CTGGAGGTGT CGGCAAAGCT	660
CTAAAATCTG TGGATCAGTA TTTGGAGCAA AATAAACTTC AAATAGGGGT TGAGGTTGAA	720
ACCAGGACAA TTGAAGAAGT ACGTGAGGTT CTAGACTATG CATCTCAAAC AAAGACTTCG	780
TTGACTAGGA TAATGCTGGA CAATATGGTT GTTCCATTAT CTAACGGAGA TATTGATGTA	840
TCCATGCTTA AGGAGGCTGT AGAATTGATC AATGGGAGGT TTGATACGGA GGCTTCAGGA	900
AATGTTACCC TTGAAACAGT ACACAAGATT GGACAAACTG GTGTTACCTA CATTTCTAGT	960
GGTGCCCTGA CGCATTCCGT GAAAGCACTT GACATTTCCC TGAAGATCGA TACAGAGCTC	1020
GCCCTTGAAG TTGGAAGGCG TACAAAACGA GCA	1053